

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Chiron Corporation
- (ii) TITLE OF INVENTION: Methods for Administration of Recombinant Gene Delivery Vehicles for Treatment of Hemophilia and Other Disorders
- (iii) NUMBER OF SEQUENCES: 83
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Chiron Corporation
 - (B) STREET: 4560 Horton Street
 - (C) CITY: Emeryville
 - (D) STATE: California
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 94608
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kruse, Norman J.
 - (B) REGISTRATION NUMBER: 35,235
 - (C) REFERENCE/DOCKET NUMBER: 1155.005
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (510) 923-3520
 - (B) TELEFAX: (510) 655-3542

(2) INFORMATION FOR SEQ ID NO:1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
GAGAGATGGG GGAGGCTAAC TGAG

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(2) INFORMATION FOR SEQ ID NO:2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
GATCCTCAGT TAGCCTCCCC CATCTCTC

28

(2) INFORMATION FOR SEQ ID NO:3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
TATATCTCCA GATGAGGTAC ATGATTTAG GCTTG

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(2) INFORMATION FOR SEQ ID NO:4:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
TATATATCGA TTCAAGGCAT TTTCTTTCA TCAATAAAAC

40

(2) INFORMATION FOR SEQ ID NO:5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
TCGAGGATCC GCCCGGGCGG CGCGATCGAT GTCGACG

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(2) INFORMATION FOR SEQ ID NO:6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
CGCGTCGACA TCGATGCGGC CGCCCGGGCG GATCC

35

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGTGAAATTAG AGCTCGGTAC CCGGGGGATCC TCTAGAGTCG ACCTGCAGGC ATGCAAGCTT 60
GGCGTAATCA TGGTCAT 77

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Arg Glu Met Gly Glu Ala Asn
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCCGAGAGAT GGGGGAGGCT AACTGAG 27

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGCTCTCTA CCCCCTCCGA TTGACACCTA G 31

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Ile Met Thr Met

1 5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCCTGTGCCT TATTTGAAC T AACC

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(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCCACCAACAA CCACATATCC CTCC

24

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCAGTCCTCC GATTGACTG

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(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGCCAGTCC TCCGATTGAC TGAGTCGCC GGGTACCGT GTATCCAATA AACCTCTTG

60

CAGTTGCATC CGACTTGTGG TCTCGCTGTT CCTTGGGAGG GTCTCCTCTG AGTGATTGAC

120

TACCCGTCAG CGGGGGTCTT TCATTTGGGG GCTCGTCCGG GATCGGGAGA CCCCTGCCA

180

GGGACCACCG ACCCACCACCC GGGAGGTAAG CTGGCCAGCA ACTTATCTGT GTCTGTCCGA

240

TTGTCTAGTG TCTATGACTG ATTTTATGCG CCTGCGTCGG TACTAGTTAG CTAACTAGCT

300

CTGTATCTGG CGGACCCGTG GTGGAACCTGA CGAGTTCGGA ACACCCGGCC GCAACCCCTGG

360

GAGACGTCCC AGGGACTTCG GGGGCCGTTT TTGTGGCCCG ACCTGAGTCC AAAAATCCCG

420

ATCGTTTTGG ACTCTTTGGT GCACCCCCCT TAGAGGAGGG ATATGTGGTT CTGGTAGGAG

480

ACGAGAACCT AAAACAGTTC CCGCCTCCGT CTGAATTGTT GCTTTCGGTT TGGGACCGAA

540

GCCGCCGCCGC GCGTCTTGTC TGCTGCAGCA TCGTTCTGTG TTGTCTCTGT CTGACTGTGT

600

TTCTGTATTT GTCTGAGAAT ATGGGCCAGA CTGTTACAC TCCCTTAAGT TTGACCTTAG

660

GTCACTGGAA AGATGTCGAG CGGATCGCTC ACAACCAGTC GGTAGATGTC AAGAAGAGAC 720
GTTGGGTTAC CTTCTGCTCT GCAGAATGGC CAACCTTAA CGTCGGATGG CCGCGAGACG 780
GCACCTTAA CCGAGACCTC ATCACCCAGG TTAAGATCAA GGTCTTTCA CCTGGCCCGC 840
ATGGACACCC AGACCAGGTC CCCTACATCG TGACCTGGGA AGCCTGGCT TTTGACCCCC 900
CTCCCTGGGT CAAGCCCTT GTACACCCTA AGCCTCCGCC TCCTCTTCCT CCATCCGCC 960
CGTCTCTCCC CCTTGAAACCT CCTCGTTCGA CCCCCGCCTCG ATCCTCCCTT TATCCAGCCC 1020
TCACTCCTTC TCTAGGCGCC AAACCTAAAC CTCAAGTTCT TTCTGACAGT GGGGGGCCGC 1080
TCATCGACCT ACTTACAGAA GACCCCCCGC CTTATAGGGA CCCAAGACCA CCCCCCTCCG 1140
ACAGGGACGG AAATGGTGGGA GAAGCGACCC CTGCGGGAGA GGCACCGGAC CCCTCCCCAA 1200
TGGCATCTCG CCTACGTGGG AGACGGGAGC CCCCTGTGGC CGACTCCACT ACCTCGCAGG 1260
CATTCCCCCT CCGCGCAGGA GGAAACGGAC AGCTTCAATA CTGGCCGTTC TCCTCTTCG 1320
ACCTTTACAA CTGGAAAAAT AATAACCCTT CTTTTCTGA AGATCCAGGT AACTGACAG 1380
CTCTGATCGA GTCTGTTCTC ATCACCCATC AGCCCACCTG GGACGACTGT CAGCAGCTGT 1440
TGGGGACTCT GCTGACCGGA GAAGAAAAAC AACGGGTGCT CTTAGAGGCT AGAAAGGCGG 1500
TGCAGGGCGA TGATGGCGC CCCACTCAAC TGCCCAATGA AGTCGATGCC GCTTTCCCC 1560
TCGAGCGCCC AGACTGGGAT TACACCACCC AGGCAGGTAG GAACCACCTA GTCCACTATC 1620
GCCAGTTGCT CCTAGCGGGT CTCCAAAACG CGGGCAGAAG CCCCACCAAT TTGGCCAAGG 1680
TAAAAGGAAT AACACAAGGG CCAATGAGT CTCCCTCGGC CTTCTAGAG AGACTTAAGG 1740
AAGCCTATCG CAGGTACACT CCTTATGACC CTGAGGACCC AGGGCAAGAA ACTAATGTGT 1800
CTATGTCTTT CATTGGCAG TCTGCCAG ACATTGGGAG AAAGTTAGAG AGGTTAGAAG 1860
ATTTAAAAAA CAAGACGCTT GGAGATTTGG TTAGAGAGGC AGAAAAGATC TTTAATAAAC 1920
GAGAAACCCC GGAAGAAAGA GAGGAACGTA TCAGGAGAGA AACAGAGGAA AAAGAAGAAC 1980
GCCGTAGGAC AGAGGATGAG CAGAAAGAGA AAGAAAGAGA TCGTAGGAGA CATAGAGAGA 2040
TGAGCAAGCT ATTGGCCACT GTCGTTAGTG GACAGAAACA GGATAGACAG GGAGGAGAAC 2100
GAAGGAGGTC CCAACTCGAT CGCGACCAGT GTGCCTACTG CAAAGAAAAG GGGCACTGGG 2160
CTAAAGATTG TCCCAAGAAA CCACGAGGAC CTCGGGGACC AAGACCCCAG ACCTCCCTCC 2220
TGACCCCTAGA TGACTAGGGGA GGTCAGGGTC AGGAGCCCCC CCCTGAACCC AGGATAACCC 2280
TCAAAGTCGG GGGCAACCC GTCACCTTCC TGGTAGATAC TGGGGCCCAA CACTCCGTGC 2340
TGACCCAAAA TCCTGGACCC CTAAGTGATA AGTCTGCCTG GGTCCAAGGG GCTACTGGAG 2400
GAAAGCGGTA TCGCTGGACC ACGGATCGCA AAGTACATCT AGCTACCGGT AAGGTCACCC 2460
ACTCTTCCT CCATGTACCA GACTGTCCCT ATCCTCTGTT AGGAAGAGAT TTGCTGACTA 2520

AACTAAAAGC CCAAATCCAC TTTGAGGGAT CAGGAGCTCA GGTTATGGGA CCAATGGGGC 2580
AGCCCCTGCA AGTGTGACC CAAATATAG AAGATGAGCA TCGGCTACAT GAGACCTCAA 2640
AAGAGCCAGA TGTTTCTCTA GGGTCCACAT GGCTGTCTGA TTTTCCTCAG GCCTGGCGG 2700
AAACCGGGGG CATGGGACTG GCAGTTCGCC AAGCTCCTCT GATCATACCT CTGAAAGCAA 2760
CCTCTACCCC CGTGTCCATA AAACAATACC CCATGTCACA AGAAGCCAGA CTGGGGATCA 2820
AGCCCCACAT ACAGAGACTG TTGGACCAGG GAATACTGGT ACCCTGCCAG TCCCCCTGGA 2880
ACACGCCCCT GCTACCCGTT AAGAAACCAG GGACTAATGA TTATAGGCCT GTCCAGGATC 2940
TGAGAGAAGT CAACAAGCGG GTGGAAGACA TCCACCCCAC CGTGCCAAC CCTTACAACC 3000
TCTTGAGCGG GCTCCCACCG TCCCACCAGT GGTACACTGT GCTTGATTTA AAGGATGCCT 3060
TTTTCTGCCT GAGACTCCAC CCCACCAGTC AGCCTCTCTT CGCCTTGAG TGGAGAGATC 3120
CAGAGATGGG AATCTCAGGA CAATTGACCT GGACCAGACT CCCACAGGGT TTCAAAAACA 3180
GTCCCACCCCT GTTGATGAG GCACTGCACA GAGACCTAGC AGACTTCCGG ATCCAGCACC 3240
CAGACTTGAT CCTGCTACAG TACGTGGATG ACTTACTGCT GGCGCCACT TCTGAGCTAG 3300
ACTGCCAACA AGGTACTCGG GCCCTGTTAC AAACCCTAGG GAACCTCGGG TATCGGGCCT 3360
CGGCCAAGAA AGCCCAAATT TGCCAGAAC AGGTCAAGTA TCTGGGTAT CTTCTAAAAG 3420
AGGGTCAGAG ATGGCTGACT GAGGCCAGAA AAGAGACTGT GATGGGGCAG CCTACTCCGA 3480
AGACCCCTCG ACAACTAAGG GAGTCCCTAG GGACGGCAGG CTTCTGTCGC CTCTGGATCC 3540
CTGGGTTTGC AGAAATGGCA GCCCCCTTGT ACCCTCTCAC CAAACGGGG ACTCTGTTA 3600
ATTGGGGCCC AGACCAACAA AAGGCTATC AAGAAATCAA GCAAGCTCTT CTAACTGCC 3660
CAGCCCTGGG GTGCCAGAT TTGACTAACG CCTTGAACT CTTTGTGAC GAGAAGCAGG 3720
GCTACGCCAA AGGTGTCTA ACGCAAAAC TGGGACCTTG GCGTCGGCCG GTGGCCTACC 3780
TGTCCAAAAA GCTAGACCCA GTAGCAGCTG GGTGGCCCCC TTGCCTACGG ATGGTAGCAG 3840
CCATTGCCGT ACTGACAAAG GATGCAGGCA AGCTAACCAT GGGACAGCCA CTAGTCATTC 3900
TGGCCCCCA TGCAGTAGAG GCACTAGTCA AACAAACCCCC CGACCGCTGG CTTTCCAACG 3960
CCCGGATGAC TCACTATCAG GCCTTGCTTT TGGACACGGA CCGGGTCCAG TTCGGACCGG 4020
TGGTAGCCCT GAACCCGGCT ACGCTGCTCC CACTGCCTGA GGAAGGGCTG CAACACAAC 4080
GCCTTGATAT CCTGGCCGAA GCCCACGGAA CCCGACCCGA CCTAACGGAC CAGCCGCTCC 4140
CAGACGCCGA CCACACCTGG TACACGGATG GAAGCAGTCT CTTACAAGAG GGACAGCGTA 4200
AGGCAGGGAGC TGCGGTGACC ACCGAGACCG AGGTAATCTG GGCTAAAGCC CTGCCAGCCG 4260
GGACATCCGC TCAGCGGGCT GAACTGATAG CACTCACCCA GGCCCTAAAG ATGGCAGAAG 4320

GTAAGAAGCT AAATGTTTAT ACTGATAGCC GTTATGCTTT TGCTACTGCC CATATCCATG 4380
GAGAAATATA CAGAAGGCGT GGGTTGCTCA CATCAGAAGG CAAAGAGATC AAAAATAAAG 4440
ACGAGATCTT GGCCCTACTA AAAGCCCTCT TTCTGCCAA AAGACTTAGC ATAATCCATT 4500
GTCCAGGACA TCAAAAGGGA CACAGGCCG AGGCTAGAGG CAACCGGATG GCTGACCAAG 4560
CGGCGGAAA GGCAGCCATC ACAGAGACTC CAGACACCTC TACCCCTCCTC ATAGAAAATT 4620
CATCACCCCTA CACCTCAGAA CATTTCATT ACAAGTGAC TGATATAAAG GACCTAACCA 4680
AGTTGGGGC CATTATGAT AAAACAAAGA AGTATTGGGT CTACCAAGGA AAACCTGTGA 4740
TGCCTGACCA GTTTACTTTT GAATTATTAG ACTTTCTTCA TCAGCTGACT CACCTCAGCT 4800
TCTCAAAAT GAAGGCTCTC CTAGAGAGAA GCCACAGTCC CTACTACATG CTGAACCGGG 4860
ATCGAACACT CAAAAATATC ACTGAGACCT GCAAAGCTTG TGCACAAGTC AACGCCAGCA 4920
AGTCTGCCGT TAAACAGGGA ACTAGGGTCC CGGGCATCG GCCCGGCACT CATTGGGAGA 4980
TCGATTCAC CGAGATAAAG CCCGGATTGT ATGGCTATAA ATATCTTCTA GTTTTTATAG 5040
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CCAAGAAGCT ACTAGAGGAG ATCTTCCCCA GGTCGGCAT GCCTCAGGTA TTGGGAACTG 5160
ACAATGGGCC TGCCTTCGTC TCCAAGGTGA GTCAGACAGT GGCGATCTG TTGGGGATTG 5220
ATTGGAAATT ACATTGTGCA TACAGACCCC AAAGCTCAGG CCAGGTAGAA AGAATGAATA 5280
GAACCATCAA GGAGACTTTA ACTAAATTAA CGCTTGCAAC TGGCTCTAGA GACTGGGTGC 5340
TCCTACTCCC CTTAGCCCTG TACCGAGCCC GCAACACGCC GGGCCCCAT GGCCTCACCC 5400
CATATGAGAT CTTATATGGG GCACCCCGC CCCTGTAAA CTTCCCTGAC CCTGACATGA 5460
CAAGAGTTAC TAACAGCCCC TCTCTCCAAG CTCACTTACA GGCTCTCTAC TTAGTCCAGC 5520
ACGAAGTCTG GAGACCTCTG GCGGAGCCT ACCAAGAACCA ACTGGACCGA CCGGTGGTAC 5580
CTCACCCCTTA CCGAGTCGGC GACACAGTGT GGGTCCGCCG ACACCAGACT AAGAACCTAG 5640
AACCTCGCTG GAAAGGACCT TACACAGTCC TGCTGACCAC CCCCACCGCC CTCAAAGTAG 5700
ACGGCATCGC AGCTTGGATA CACGCCGCC ACGTGAAGGC TGCCGACCCC GGGGGTGGAC 5760
CATCCTCTAG ACTGACATGG CGCGTTCAAC GCTCTAAAA CCCCTTAAAA ATAAGGTTAA 5820
CCCGCGAGGC CCCCTAATCC CCTTAATTCT TCTGATGCTC AGAGGGTCA GTACTGCTTC 5880
GCCCGGCTCC AGTCCTCATC AAGTCTATAA TATCACCTGG GAGGTAACCA ATGGAGATCG 5940
GGAGACGGTA TGGGCAACTT CTGGCAACCA CCCTCTGTGG ACCTGGTGGC CTGACCTTAC 6000
CCCAGATTAA TGTATGTTAG CCCACCATGG ACCATCTTAT TGGGGGCTAG AATATCAATC 6060
CCCTTTTCT TCTCCCCGG GGCCCCCTTG TTGCTCAGGG GGCAGCAGCC CAGGCTGTC 6120
CAGAGACTGC GAAGAACCTT TAACCTCCCT CACCCCTCGG TGCAACACTG CCTGGAACAG 6180

ACTCAAGCTA GACCAGACAA CTCATAAATC AAATGAGGGA TTTTATGTTT GCCCCGGGCC 6240
CCACCGCCCC CGAGAATCCA AGTCATGTGG GGGTCCAGAC TCCTTCTACT GTGCCTATTG 6300
GGGCTGTGAG ACAACCAGTA GAGCTTACTG GAAGCCCTCC TCATCATGGG ATTCATCAC 6360
AGTAAACAAAC AATCTCACCT CTGACCAGGC TGTCCAGGTA TGCAAAGATA ATAAGTGGTG 6420
CAACCCCTTA GTTATTTCGGT TTACAGACGC CGGGAGACGG GTTACTTCCT GGACCACAGG 6480
ACATTACTGG GGCTTACGTT TGTATGTCTC CGGACAAGAT CCAGGGCTTA CATTGGGAT 6540
CCGACTCAGA TACCAAAATC TAGGACCCCG CGTCCAATA GGGCCAAACC CCGTTCTGGC 6600
AGACCAACAG CCACTCTCCA AGCCCAAACC TGTTAAGTCG CCTTCAGTCA CCAAACCACC 6660
CAGTGGGACT CCTCTCTCCC CTACCCAACT TCCACCGGCG GGAACGGAAA ATAGGCTGCT 6720
AAACTTAGTA GACGGAGCCT ACCAAGCCCT CAACCTCACC AGTCCTGACA AAACCCAAGA 6780
GTGCTGGTTG TGTCTAGTAG CGGGACCCCC CTACTACGAA GGGGTTGCCG TCCTGGGTAC 6840
CTACTCCAAC CATACTCTG CTCCAGCCAA CTGCTCCGTG GCCTCCCAAC ACAAGTTGAC 6900
CCTGTCCGAA GTGACCGGAC AGGGACTCTG CATAGGAGCA GTTCCAAAAA CACATCAGGC 6960
CCTATGTAAT ACCACCCAGA CAAGCAGTCG AGGGTCCTAT TATCTAGTTG CCCCTACAGG 7020
TACCATGTGG GCTTGTAGTA CCGGGCTTAC TCCATGCATC TCCACCACCA TACTGAACCT 7080
TACCACTGAT TATTGTGTTT TTGTCGAACT CTGGCCAAGA GTCACCTATC ATTCCCCAG 7140
CTATGTTAC GGCCTGTTG AGAGATCCAA CCGACACAAA AGAGAACCGG TGCGTTAAC 7200
CCTGGCCCTA TTATTGGGTG GACTAACCAT GGGGGAAATT GCCGCTGGAA TAGGAACAGG 7260
GACTACTGCT CTAATGCCA CTCAGCAATT CCAGCAGCTC CAAGCCGCAG TACAGGATGA 7320
TCTCAGGGAG GTTAAAAAAT CAATCTCTAA CCTAGAAAAG TCTCTCACTT CCCTGTCTGA 7380
AGTTGTCCTA CAGAATCGAA GGGGCCTAGA CTTGTTATTT CTAAAAGAAG GAGGGCTGTG 7440
TGCTGCTCTA AAAGAAGAAT GTTGCTTCTA TGCGGACCAC ACAGGACTAG TGAGAGACAG 7500
CATGGCCAAA TTGAGAGAGA GGCTTAATCA GAGACAGAAA CTGTTTGAGT CAACTCAAGG 7560
ATGGTTGAG GGACTGTTTA ACAGATCCCC TTGGTTTACC ACCTTGATAT CTACCATTAT 7620
GGGACCCCTC ATTGTACTCC TAATGATTCTT GCTCTTCGGA CCCTGCATTC TTAATCGATT 7680
AGTCCAATTT GTTAAAGACA GGATATCAGT GGTCCAGGCT CTAGTTTGA CTCAACAATA 7740
TCACCAGCTG AAGCCTATAG AGTACGAGCC ATAGATAAAA TAAAAGATTT TATTTAGTCT 7800
CCAGAAAAAG GGGGAATGA AAGACCCAC CTGTAGGTTT GGCAAGCTAG CTTAAGTAAC 7860
GCCATTTCG AAGGCATGGA AAAATACATA ACTGAGAATA GAGAAGTTCA GATCAAGGTC 7920
AGGAACAGAT GGAACAGCTG AATATGGGCC AAACAGGATA TCTGTGGTAA GCAGTTCCCTG 7980

CCCCGGCTCA	GGGCAAGAA	CAGATGGAAC	AGCTGAATAT	GGGCCAAACA	GGATATCTGT	8040
GGTAAGCAGT	TCCTGCCCG	GCTCAGGGCC	AAGAACAGAT	GGTCCCCAGA	TGCGGTCCAG	8100
CCCTCAGCAG	TTTCTAGAGA	ACCATCAGAT	GTTCAGGG	TGCCCAAGG	ACCTGAAATG	8160
ACCCTGTGCC	TTATTTGAAC	TAACCAATCA	GTTCGCTTCT	CGCTTCTGTT	CGCGCGCTTC	8220
TGCTCCCCGA	GCTCAATAAA	AGAGCCCACA	ACCCCTCACT	CGGGGCGCCA	GTCCTCCGAT	8280
TGACTGAGTC	GCCCAGGTAC	CCGTGTATCC	AATAAACCT	CTTGCAGTTG	CA	8332

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGGAGTGGTA ACAGTCTGGC CTTAATTCTC AG

32

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGGTCGACCT CGAGAATTAA TTC

23

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTGGGAGACG TCCCAGGGAC TTC

23

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGCCAGACTG TTACCACTCC CTGAAGTTG AC

32

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATCGATAAA ATAAAAGATT TTATTTAGTC

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(2) INFORMATION FOR SEQ ID NO:21:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
CAAATGAAAG ACCCCCGCTG AC

22

(2) INFORMATION FOR SEQ ID NO:22:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
GAAGCTTCTC CCAGAACCA CCAGTCTTGA AACGCCATC

39

(2) INFORMATION FOR SEQ ID NO:23:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
GTACCAAGCTT TTGGTCTCAT CAAAG

25

(2) INFORMATION FOR SEQ ID NO:24:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
CTCCTCGAGC TAAAGATATT TTAGAGAAGA ATTAAC

36

(2) INFORMATION FOR SEQ ID NO:25:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
TTCCTCTGGA CAGCTGTCTA CTTTG

25

(2) INFORMATION FOR SEQ ID NO:26:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
TCGAGGGGCC CAGATCTGCG GCCGCTCGCG AGTCGACAAG CTTGGATCCA T

51

(2) INFORMATION FOR SEQ ID NO:27:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
CGATGGATCC AAGCTTGTCTG ACTCGCGAGC GGCCGCAGAT CTGGGGCCCC 49

(2) INFORMATION FOR SEQ ID NO:28:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
CACCGTCGTC GACTTATGCT 20

(2) INFORMATION FOR SEQ ID NO:29:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
GACCGTCGAC TCAATTCTGG GAGAAGCTTC TTGG 34

(2) INFORMATION FOR SEQ ID NO:30:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
CACCGTCGTC GACTTATGCT 20

(2) INFORMATION FOR SEQ ID NO:31:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
CAACGCTCGA GAAGCAGAAAT CGCAAAAGGC 30

(2) INFORMATION FOR SEQ ID NO:32:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
TCGGCTCGAG GCATCAACGG GAAATAACTC GT 32

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCGACTCGAG TCAGTAGAGG TCCTGTGCCT C

31

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCGACTCGAG CATGGGGCCC TGGGGC

26

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCACTGGAAT TCGTCAGGGC G

21

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGCGCCGCTC GAGTCTACAA TGGCCTTGAC CTTTGCTTTA CTGG

44

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGCCCATCG ATTCAATTCT TACTTCTTAA ACTTTCTTGC AAG

43

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGCGCCGCTC GAGCATCCAA TGGCCCTGTC CTTTTCTTTA CTTATGG

47

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCATCGATT C AATCCTTCCT CCTTAATCTT TTTTGCAAG 39

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCGGATCCTC TACAATGGCC TTGACCTTG CTTTACTGG 39

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CGCGCCGGCG GCCGCTCATT CCTTACTTCT TAAACTTCT TGCAAG 46

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCGGATCCCA TCCAATGGCC CTGTCCTTT CTTTACTTAT GG 42

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGCGCCGGCG GCCGCTCAAT CCTCCTCCT TAATCTTT TGCAAG 46

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9080 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGGGGGGGGG GGGGGGGGGG GGGTGAGCAC ATCCAGTGGG TAAAGTTCCT TAAAATGCTC 60
TGCAAAGAAA TTGGGACTTT TCATTAATC AGAAATTAA CTTTTTCCC CTCCTGGGAG 120
CTAAAGATAT TTAGAGAAG AATTAACCTT TTGCTTCTCC AGTTGAACAT TTGTAGCAAT 180

AAGTCATGCA	AATAGAGCTC	TCCACCTGCT	TCTTTCTGTG	CCTTTTGCAG	TTCTGCTTTA	240
GTGCCACCG	AAGATACTAC	CTGGGTGCAG	TGGAACTGTC	ATGGGACTAT	ATGCAAAGTG	300
ATCTCGGTGA	GCTGCCTGTG	GACGCAAGAT	TTCCTCCTAG	AGTGCCAAAA	TCTTTCCAT	360
TCAACACCTC	AGTCGTGTAC	AAAAAGACTC	TGTTTGTAGA	ATTACCGAT	CACCTTTCA	420
ACATCGCTAA	GCCAAGGCCA	CCCTGGATGG	GTCTGCTAGG	TCCTACCATC	CAGGCTGAGG	480
TTTATGATAC	AGTGGTCATT	ACACTTAAGA	ACATGGCTTC	CCATCCTGTC	AGTCTTCATG	540
CTGTTGGTGT	ATCCTACTGG	AAAGCTTCTG	AGGGAGCTGA	ATATGATGAT	CAGACAGTC	600
AAAGGGAGAA	AGAAGATGAT	AAAGCTTCC	CTGGTGGAAAG	CCATACATAT	GTCTGGCAGG	660
TCCTGAAAGA	GAATGGTCCA	ATGCCCTCTG	ACCCACTGTG	CCTTACCTAC	TCATATCTT	720
CTCATGTGGA	CCTGGTAAAAA	GACTXGAATT	CAGGCCTCAT	TGGAGGCCCTA	CTAGTATGTA	780
GAGAAGGGAG	TCTGGCCAAG	AAAAAGACAC	AGACCTTGCA	CAAATTATA	CTACTTTTG	840
CTGTATTGTA	TGAAGGGAAA	AGTTGGCACT	CAGAAACAAA	GAACTCCTTG	ATGCAGGATA	900
GGGATGCTGC	ATCTGCTCGG	GCCTGGCCTA	AAATGCACAC	AGTCATGGT	TATGAAACA	960
GGTCTCTGCC	AGGTCTGATT	GGATGCCACA	GGAAATCAGT	CTATTGGCAT	GTGATTGGAA	1020
TGGGCACCAC	TCCTGAAGTG	CACTCAATAT	TCCCTGAAGG	TCACACATTT	CTTGTGAGGA	1080
ACCATCGCCA	GGCGTCCCTG	GAAATCTCGC	CAATAACTTT	CCTTACTGCT	CAAACACTCT	1140
TGATGGACCT	TGGACAGTTT	CTACTGTTT	GTCATATCTC	TTCCACCAA	CATGATGGCA	1200
TGGAAGCTTA	TGTCAAAGTA	GACAGCTGTC	CAGAGGAACC	CCAACTACGA	ATGAAAAATA	1260
ATGAAGAAGC	GGAAGACTAT	GATGATGATC	TTACTGATTC	TGAAATGGAT	GTGGTCAGGT	1320
TTGATGATGA	CAACTCTCCT	TCCTTTATCC	AAATTGCTC	AGTTGCCAAG	AAGCATCCTA	1380
AAACTTGGGT	ACATTACATT	GCTGCTGAAG	AGGAGGACTG	GGACTATGCT	CCCTTAGTCC	1440
TCGCCCCCGA	TGACAGAAGT	TATAAAAGTC	ATATTTGAA	CAATGGCCCT	CAGCGGATTG	1500
GTAGGAAGTA	CAAAAAAGTC	CGATTATGG	CATACACAGA	TGAAACCTTT	AAGACTCGTG	1560
AAGCTATTCA	GCATGAATCA	GGAACTTGG	GACCTTTACT	TTATGGGAA	GTTGGAGACA	1620
CACTGTTGAT	TATATTTAAG	AATCAAGCAA	GCAGACCATA	TAACATCTAC	CCTCACGGAA	1680
TCACTGATGT	CCGTCTTTG	TATTCAAGGA	GATTACAAA	AGGTGTAAAA	CATTGAAAGG	1740
ATTTCCAAT	TCTGCCAGGA	AAAATATTCA	AATATAAAATG	GACAGTGA	GTAGAAGATG	1800
GGCCAACCTAA	ATCAGATCCT	CGGTGCTGTA	CCCGCTATTA	CTCTAGTTTC	GTAAATATGG	1860
AGAGAGATCT	AGCTTCAGGA	CTCATTGGCC	CTCTCCTCAT	CTGCTACAAA	GAATCTGTAG	1920
ATCAAAGAGG	AAACCAGATA	ATGTCAGACA	AGAGGAATGT	CATCCTGTT	TCTGTATTTG	1980
ATGAGAACCG	AAGCTGGTAC	CTCACAGAGA	ATATACAACG	CTTTCTCCCC	AATCCAGCTG	2040
GAGTGCAGCT	TGAGGATCCA	GAGTCCAAG	CCTCCAACAT	CATGCACAGC	ATCAATGGCT	2100
ATGTTTTGTA	TAGTTGCA	TTGTCAGTTT	TTTGCATGA	GGTGGCATA	TGGTACATTC	2160
TAAGCATTGG	AGCACAGACT	GAATTCTTT	CTGTCTTCTT	CTCTGGATAT	ACCTTCAAAC	2220
ACAAAATGGT	CTATGAAGAC	ACACTCACCC	TATTCCCATT	CTCAGGAGAA	ACTGTCTCA	2280
TGTCGATGGA	AAACCCAGGT	CTATGGATTC	TGGGGTGCCA	CAACTCAGAC	TTTCGGAACA	2340
GAGGCATGAC	CGCCTTACTG	AAGGTTTCTA	TTTGTGACAA	GAACACTGGT	GATTATTACG	2400
AGGACAGTTA	TGAAGATATT	TCAGCATACT	TGCTGAGTAA	AAACAATGCC	ATTGAACCAA	2460
GAAGCTTCTC	CCAGAATTCA	AGACACCCCTA	GCACCTAGGCA	AAAGCAATT	AATGCCACCA	2520
CAATTCCAGA	AAATGACATA	GAGAAAGACTG	ACCCCTGGTT	TGCACACAGA	ACACCTATGC	2580
CTAAAATACA	AAATGTCTCC	TCTAGTGA	TGTTGATGCT	CTTGCACAG	AGTCCTACTC	2640
CACATGGGCT	ATCCTTATCT	GATCTCCAAG	AAGCCAAATA	TGAGACTTTT	TCTGATGATC	2700
CATCACCTGG	AGCAATAGAC	AGTAATAACA	GCCTGCTGTA	AATGACACAC	TTCAGGCCAC	2760
AGCTCCATCA	CAGTGGGGAC	ATGGTATTAA	CCCCTGAGTC	AGGCCTCCAA	TAAAGATTAA	2820
ATGAGAAACT	GGGGACAACT	GCAGCAACAG	AGTTGAAGAA	ACTTGATTT	AAAGTTCTA	2880
GTACATCAAA	TAATCTGATT	TCAACAAATT	CATCAGACAA	TTTGGCAGCA	GGTACTGATA	2940
ATACAAGTT	CTTAGGACCC	CCAAGTATGC	CAGTCATTA	TGATAGTC	TTAGATACCA	3000
CTCTATTGGA	CAAAAAGTC	TCTCCCTTA	CTGAGTCTG	TGGACCTCTG	AGCTTGAGTG	3060
AAGAAAATAA	TGATTCAAAG	TTGTTAGAAT	CAGGTTAAAT	GAATGCCAA	GAAAGTTCAT	3120
GGGGAAAAAA	TGTATCGTCA	ACAGAGAGTG	GTAGGTTATT	TAAAGGGAAA	AGAGCTCATG	3180
GACCTGCTTT	GTGACTAAA	GATAATGCC	TATTCAAAGT	TAGCATCTCT	TTGTTAAAGA	3240
CAAACAAAAC	TTCCAATAAT	TCAGCAACTA	ATAGAAAGAC	TCACATTGAT	GGCCCATCAT	3300
TATTAATTGA	GAATAGTCCA	TCAGTCTGGC	AAAATATATT	AGAAAGTGAC	ACTGAGTTA	3360
AAAAAGTGAC	ACCTTTGATT	CATGACAGAA	TGCTTATGGA	CAAAATGCT	ACAGCTTGA	3420
GGCTAAATCA	TATGTCAAAT	AAAACTACTT	CATCAAAAAA	CATGGAATG	GTCCAACAGA	3480
AAAAAGAGGG	CCCCATTCCA	CCAGATGCA	AAAATCCAGA	TATGTCGTT	TTAAGATGC	3540
TATTCTGCC	AGAATCAGCA	AGGTGGATAC	AAAGGACTCA	TGGAAAGAAC	TCTCTGA	3600
CTGGGCAAGG	CCCCAGTCCA	AAGCAATTAG	TATCCTTAGG	ACCAGAAAAA	TCTGTGAAAG	3660
GTCAGAATT	CTTGTCTGAG	AAAAACAAAG	TGGTAGTAGG	AAAGGGTGAA	TTTACAAAGG	3720
ACGTAGGACT	CAAAGAGATG	GTTTTCCAA	GCAGCAGAAA	CCTATTCTT	ACTAACTTGG	3780
ATAATTACAA	TGAAAATAAT	ACACACAATC	AAGAAAAAAA	AATTCAAGGAA	GAAATAGAAA	3840

AGAAGGAAAC	ATTAATCCAA	GAGAATGTAG	TTTTGCCTCA	GATACATACA	GTGACTGGCA	3900
CTAAGAATT	CATGAAGAAC	CTTTCTTAC	TGAGCACTAG	GCAAAATGTA	GAAGGTTCAT	3960
ATGACGGGGC	ATATGCTCCA	GTACTTCAAG	ATTTTAGGTC	ATTAATGAT	TCAACAAATA	4020
GAACAAAGAA	ACACACAGCT	CATTTCTCAA	AAAAAGGGGA	GGAAGAAAAC	TTGGAAGGCT	4080
TGGGAAATCA	AACCAAGCAA	ATTGTAGAGA	ATATGCATG	CACCCACAAGG	ATATCTCTA	4140
ATACAAGCCA	GCAGAATT	GTCACGCAAC	GTAGTAAGAG	AGCTTGAAA	CAATTCAAGAC	4200
TCCCCTAGA	AGAAACAGAA	CTTGAAAAAA	GGATAATTGT	GGATGACACC	TCAACCCAGT	4260
GGTCCAAAAA	CATGAAACAT	TTGACCCCGA	GCACCCCTCAC	ACAGATAGAC	TACAATGAGA	4320
AGGAGAAAGG	GGCCATTACT	CACTCTCCCT	TATCAGATG	CCTTACGAGG	AGTCATAGCA	4380
TCCCCTCAAGC	AAATAGATCT	CCATTACCCA	TTGCAAAGGT	ATCATCATTT	CCATCTATTA	4440
GACCTTATA	TCTGACCAGG	GTCCTATTCC	AAGACAACCT	TTCTCATCTT	CCAGCAGCAT	4500
CTTATAGAAA	GAAAGATTCT	GGGGTCCAAG	AAAGCAGTCA	TTTCTTACAA	GGAGCCAAA	4560
AAAATAACCT	TTCTTTAGCC	ATTCTAACCT	TGGAGATGAC	TGGTGTCAA	AGAGAGGTTG	4620
GCTCCCTGGG	GACAAGTGCC	ACAAATTCA	TCACATACAA	GAAAGTTGAG	AAACACTGTT	4680
TCCCAGAAACC	AGACTTGCCC	AAAACATCTG	GCAAAGTTGA	ATTGCTTCCA	AAAGTTCAC	4740
TTTATCAGAA	GGACCTATT	CCTACGGAAA	CTAGCAATGG	GTCTCTGGC	CATCTGGATC	4800
TCGTGGAAGG	GAGCCTTCTT	CAGGGAACAG	AGGGAGCGAT	TAAGTGGAA	GAAGCAAACA	4860
GACCTGGAAA	AGTTCCCTT	CTGAGAGTAG	CAACAGAAAG	CTCTGCAAAG	ACTCCCTCCA	4920
AGCTATTGGA	TCCTCTTGCT	TGGGATAACC	ACTATGGTAC	TCAGATACCA	AAAGAAGAGT	4980
GGAAATCCCA	AGAGAAGTCA	CCAGAAAAAA	CAGCTTTAA	GAAAAGGGAT	ACCATTTGT	5040
CCCTGAACGC	TTGTGAAAGC	AATCATGAA	TAGCAGCAAT	AAATGAGGGA	CAAATAAGC	5100
CCGAAATAGA	AGTCACCTGG	GCAAAGCAAG	GTAGGACTGA	AAGGCTGTGC	TCTCAAACCC	5160
CACCAGTCTT	GAAACGCCAT	CAACGGAAA	TAACTCGTAC	TACTCTTCAG	TCAGATCAAG	5220
AGGAAATTGA	CTATGATGAT	ACCATATCA	TTGAAATGAA	GAAGGAAGAT	TTTGACATTT	5280
ATGATGAGGA	TGAAAATCA	AGCCCCCGCA	GCTTCAAAAA	GAAAACACGA	CACTATT	5340
TTGCTGCAGT	GGAGAGGCTC	TGGGATTATG	GGATGAGTAG	CTCCCCACAT	GTTCTAAGAA	5400
ACAGGGCTCA	GAGTGGCAGT	GTCCCTCAGT	TCAAGAAAGT	TGTTTCCAG	GAATTACTG	5460
ATGGCTCCTT	TACTCAGCCC	TTATACCGTG	GAGAACTAAA	TGAACATTTG	GGACTCCTGG	5520
GGCCATATAT	AAGAGCAGAA	GTTGAAGATA	ATATCATGGT	AACTTCAGA	AATCAGGCC	5580
CTCGTCCCTA	TTCCTTCTAT	TCTAGCCTTA	TTTCTTATGA	GGAAGATCAG	AGGCAAGGAG	5640
CAGAACCTAG	AAAAAAACTT	GTCAAGCCTA	ATGAAACCAA	AACTACTTT	TGGAAAGTGC	5700
AAACATCATAT	GGCACCCACT	AAAGATGAGT	TTGACTGCAA	AGCCTGGGCT	TATTTCTCTG	5760
ATGTTGACCT	GGAAAAAGAT	GTGCACTCAG	GCCTGATTGG	ACCCCTCTG	GTCTGCCACA	5820
CTAACACACT	GAACCCGTGCT	CATGGGAGAC	AAAGTACAGT	ACAGGAATT	GCTCTGTTT	5880
TCACCACATTT	TGATGAGACC	AAAAGCTGGT	ACTTCACTGA	AAATATGGAA	AGAAACTGCA	5940
GGGCTCCCTG	CAATATCCAG	ATGGAAGATC	CCACTTTAA	AGAGAATTAT	CGCTTCCATG	6000
CAATCAATGG	CTACATAATG	GATACACTAC	CTGGCTTAGT	AATGGCTCAG	GATCAAAGGA	6060
TTCGATGGTA	TCTGCTCAGC	ATGGGCAGCA	ATGAAAACAT	CCATCTATT	CATTTCTAGT	6120
GACATGTGTT	CACTGTACGA	AAAAAAAGAGG	AGTATAAAAT	GGCACTGTAC	AATCTCTATC	6180
CAGGTGTTTT	TGAGACAGTG	GAAATGTTAC	CATCCAAAGC	TGGAATTGG	CGGGTGGAA	6240
GCCTTATTGG	CGAGCATCTA	CATGCTGGGA	TGAGCACACT	TTTCTGGTG	TACAGCAATA	6300
AGTGTAGAC	TCCCCTGGGA	ATGGCTTCTG	GACACATTAG	AGATTTTCAG	ATTACAGCTT	6360
CAGGACAATA	TGGACAGTGG	GCCCCAAAGC	TGGCCAGACT	TCATTATTCC	GGATCAATCA	6420
ATGCCTGGAG	CACCAAGGAG	CCCTTTCTT	GGATCAAGGT	GGATCTGGT	GCACCAATGA	6480
TTATTACCGG	CATCAAGACC	CAGGGTGC	GTCAGAAGTT	CTCCAGCCTC	TACATCTCTC	6540
AGTTTATCAT	CATGTATAGT	CTTGATGGGA	AGAAGTGGCA	GACTTATCGA	GGAAATTCCA	6600
CTGGAACCTT	AATGGTCTTC	TTTGGCAATG	TGGATTTCATC	TGGGATAAAA	CACAATATT	6660
TTAACCCCTCC	AATTATTGCT	CGATACATCC	GTGGCACC	AACTCATTAT	AGCATTGCA	6720
GCACTCTTCG	CATGGAGTTG	ATGGGCTGTG	ATTTAAATAG	TTGCACTGATG	CCATTGGGAA	6780
TGGAGAGTAA	AGCAATATCA	GATGCACAGA	TTACTGCTC	ATCCTACTTT	ACCAATATGT	6840
TTGCCACCTG	GTCTCTTCA	AAAGCTCGAC	TTCACCTCCA	AGGGAGGAGT	ATGCTGGGA	6900
GACCTCAGGT	GAATAATCCA	AAAGAGTGGC	TGCAAGTGG	CTTCCAGAAG	ACAATGAAAG	6960
TCACAGGAGT	AACTACTCAG	GGAGTAAAAT	CTCTGTTAC	CAGCATGTAT	GTGAAGGAGT	7020
TCCTCATCTC	CAGCAGTC	GATGCC	AGTGGACTCT	CTTTTTCA	AATGGCAAAG	7080
TAAAGGTTT	TCAGGGAAAT	CAAGACTCT	TCACACCTGT	GGTGAACCT	CTAGACCCAC	7140
CGTTACTGAC	TCGCTACCTT	CGAACATCC	CCCAGAGTTG	GGTGCAC	ATTGCCCTGA	7200
GGATGGAGGT	TCTGGGCTGC	GAGGCACAGG	ACCTCTACTG	AGGGTGGCCA	CTGCAGCACC	7260
TGCCACTGCC	GTCACCTCTC	CCTCC	TCCAGGGCAG	TGTCCTCCC	TGGCTTGCC	7320
TCTACCTTTG	TGCTAAATCC	TAGCAGACAC	TGCCTGAAG	CCTCC	TAACTATCAT	7380
CAGTCCTGCA	TTTCTTTGGT	GGGGGCCAG	GAGGGTGCAT	CCAATTAAAC	TTAACTCTTA	7440
CCTATT	GCAGCTGCTC	CCAGATTACT	CCTCC	AATATAACTA	GGCAAAAGA	7500

AGTGAGGAGA AACCTGCATG AAAGCATTCT TCCCTGAAAA GTTAGGCCTC TCAGACTCAC	7560
CACTTCCTCT GTTGTAGAAA AACTATGTGA TGAAACTTGTG AAAAAGATAT TTATGATGTT	7620
AACATTCAG GTTAAGCCTC ATACGTTAA AATAAAACTC TCAGTTGTTT ATTATCCTGA	7680
TCAAGCATGG AACAAAGCAT GTTTCAAGGAT CAGATCAATA CAATCTGGA GTCAAAAGGC	7740
AAATCATTG GACAATCTGC AAAATGGAGA GAATACAATA ACTACTACAG TAAAGCTGT	7800
TTCTGCTTC TTACACATAG ATATAATTAT GTTATTAGT CATTATGAGG GGCACATCT	7860
TATCTCCAAA ACTAGCATTG TTAAACTGAG AATTATAGAT GGGGTTCAAG AATCCCTAAG	7920
TCCCCTGAAA TTATATAAGG CATTCTGTAT AAATGCAAAT GTGCATTTT CTGACGAGTG	7980
TCCATAGATA TAAAGGCATT TGGCTTAAT TCTGACCAAT AAAAATAA GTCAGGAGGA	8040
TGCAATTGTT GAAAGCTTG AAATAAAATA ACAATGCTT CTTGAAATTG GTGATGGCCA	8100
AGAAAGAAAA TGATGATGAC ATTAGGCTTC TAAAGGACAT ACATTTAATA TTTCTGTGGA	8160
AATATGAGGA AAATCCATGG TTATCTGAGA TAGGAGATAC AAACCTTGTA ATTCTAATAA	8220
TGCACTCAGT TTACTCTCTC CCTCTACTAA TTTCCTGCTG AAAATAACAC AACAAAAATG	8280
TAACAGGGGA AATTATATAC CGTGACTGAA AACTAGAGTC CTACTTACAT AGTTGAAATA	8340
TCAAGGAGGT CAGAAGAAAA TTGGACTGGT GAAAACAGAA AAAACACTCC AGTCTGCCAT	8400
ATCACCCACAC AATAGGATCC CCCTTCTTGC CCTCCACCCC CATAAGATTG TGAAGGGTTT	8460
ACTGCTCCTT CCATCTGCC GACCCCTTCA CTATGACTAC ACAGAATCTC CTGATAGTAA	8520
AGGGGGCTGG AGGCAAGGAT AAGTTATAGA GCAGTTGGAG GAAGCATCCA AAGATTGCAA	8580
CCCAGGGCAA ATGGAAAACA GGAGATCCTA ATATGAAAGA AAAATGGATC CCAATCTGAG	8640
AAAAGGCAAA AGAATGGCTA CTTTTTCTA TGCTGGAGTA TTTTCTAATA ATCCTGCTTG	8700
ACCCCTATCT GACCTCTTG GAAACTATAA CATAGCTGTC ACAGTATAGT CACAATCCAC	8760
AAATGATGCA GGTGCAAATG GTTTATAGCC CTGTGAAGTT CTTAAAGTTT AGAGGCTAAC	8820
TTACAGAAAT GAATAAGTT TTTTGTGTTA TAGCCCGGTA GAGGAGTTAA CCCCCAAAGGT	8880
GATATGGTTT TATTTCTGT TATGTTAAC TTAATAATCT TATTTTGGCA TTCTTTCCC	8940
ATTGACTATA TACATCTCTA TTTCTCAAAT GTTCATGGAA CTAGCTCTT TATTTTCTG	9000
CTGGTTTCTT CAGTAATGAG TTAAATAAAA CATTGACACA TACAAAAAAA AAAAAAAA	9060
AAAAAAAAA AAAAAAAA	9080

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2351 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe			
1	5	10	15

Cys Phe Ser Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser			
20	25	30	

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg			
35	40	45	

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val			
50	55	60	

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile			
65	70	75	80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln			
85	90	95	

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser			
100	105	110	

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser			
115	120	125	

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
130 135 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145 150 155 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
180 185 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
290 295 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305 310 315 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
325 330 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
340 345 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
370 375 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385 390 395 400

Trp Val His Tyr Ile Ala Ala Glu Glu Asp Trp Asp Tyr Ala Pro
405 410 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
420 425 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
435 440 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu

450

455

460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465 470 475 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
500 505 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
515 520 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
530 535 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545 550 555 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
565 570 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
580 585 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
595 600 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
610 615 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625 630 635 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
645 650 655

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
660 665 670

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
675 680 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
690 695 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705 710 715 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
725 730 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
740 745 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Pro
755 760 765

Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp
770 775 780

Ile Glu Lys Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys
785 790 795 800

Ile Gln Asn Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser
805 810 815

Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr
820 825 830

Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
835 840 845

Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly
850 855 860

Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu
865 870 875 880

Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
885 890 895

Val Ser Ser Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn
900 905 910

Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met
915 920 925

Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys
930 935 940

Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu
945 950 955 960

Asn Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu
965 970 975

Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe
980 985 990

Lys Gly Lys Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala
995 1000 1005

Leu Phe Lys Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser Asn
1010 1015 1020

Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser Leu Leu
1025 1030 1035 1040

Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser Asp Thr
1045 1050 1055

Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp
1060 1065 1070

Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr
1075 1080 1085

Ser Ser Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile
1090 1095 1100

Pro Pro Asp Ala Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe
1105 1110 1115 1120

Leu Pro Glu Ser Ala Arg Trp Ile Gln Arg Thr His Gly Lys Asn Ser
1125 1130 1135

Leu Asn Ser Gly Gln Gly Pro Ser Pro Lys Gln Leu Val Ser Leu Gly
1140 1145 1150

Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu Ser Glu Lys Asn Lys
1155 1160 1165

Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly Leu Lys Glu
1170 1175 1180

Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp Asn
1185 1190 1195 1200

Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu
1205 1210 1215

Ile Glu Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln
1220 1225 1230

Ile His Thr Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu
1235 1240 1245

Leu Ser Thr Arg Gln Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala
1250 1255 1260

Pro Val Leu Gln Asp Phe Arg Ser Leu Asn Asp Ser Thr Asn Arg Thr
1265 1270 1275 1280

Lys Lys His Thr Ala His Phe Ser Lys Lys Gly Glu Glu Glu Asn Leu
1285 1290 1295

Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val Glu Lys Tyr Ala Cys
1300 1305 1310

Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe Val Thr Gln
1315 1320 1325

Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu Thr
1330 1335 1340

Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser
1345 1350 1355 1360

Lys Asn Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr
1365 1370 1375

Asn Glu Lys Glu Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys
1380 1385 1390

Leu Thr Arg Ser His Ser Ile Pro Gln Ala Asn Arg Ser Pro Leu Pro
1395 1400 1405

Ile Ala Lys Val Ser Ser Phe Pro Ser Ile Arg Pro Ile Tyr Leu Thr
1410 1415 1420

Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro Ala Ala Ser Tyr

1425 1430 1435 1440

Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu Gln Gly
1445 1450 1455

Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr
1460 1465 1470

Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser
1475 1480 1485

Val Thr Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu
1490 1495 1500

Pro Lys Thr Ser Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr
1505 1510 1515 1520

Gln Lys Asp Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser Pro Gly His
1525 1530 1535

Leu Asp Leu Val Glu Gly Ser Leu Leu Gln Gly Thr Glu Gly Ala Ile
1540 1545 1550

Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys Val Pro Phe Leu Arg Val
1555 1560 1565

Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu Leu Asp Pro Leu
1570 1575 1580

Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Trp Lys
1585 1590 1595 1600

Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Asp Thr
1605 1610 1615

Ile Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile
1620 1625 1630

Asn Glu Gly Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln
1635 1640 1645

Gly Arg Thr Glu Arg Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg
1650 1655 1660

His Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu
1665 1670 1675 1680

Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe
1685 1690 1695

Asp Ile Tyr Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys
1700 1705 1710

Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr
1715 1720 1725

Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly
1730 1735 1740

Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly
1745 1750 1755 1760

Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly
1765 1770 1775

Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val
1780 1785 1790

Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu
1795 1800 1805

Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn
1810 1815 1820

Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His
1825 1830 1835 1840

His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr
1845 1850 1855

Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly
1860 1865 1870

Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg
1875 1880 1885

Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu
1890 1895 1900

Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala
1905 1910 1915 1920

Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg
1925 1930 1935

Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val
1940 1945 1950

Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser
1955 1960 1965

Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val
1970 1975 1980

Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly
1985 1990 1995 2000

Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg
2005 2010 2015

Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr Leu
2020 2025 2030

Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser
2035 2040 2045

Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln
2050 2055 2060

Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala
2065 2070 2075 2080

Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala
 2085 2090 2095
 Pro Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe
 2100 2105 2110
 Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly
 2115 2120 2125
 Lys Lys Trp Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val
 2130 2135 2140
 Phe Phe Gly Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn
 2145 2150 2155 2160
 Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser
 2165 2170 2175
 Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser
 2180 2185 2190
 Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln
 2195 2200 2205
 Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro
 2210 2215 2220
 Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro
 2225 2230 2235 2240
 Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr
 2245 2250 2255
 Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr
 2260 2265 2270
 Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His
 2275 2280 2285
 Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly
 2290 2295 2300
 Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu
 2305 2310 2315 2320
 Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile
 2325 2330 2335
 Ala Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr
 2340 2345 2350

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4832 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTCGAGCTAA AGATATTTA GAGAAGAATT AACCTTTGC TTCTCCAGTT GAACATTGT

AGCAATAAGT	CATGCAAATA	GAGCTCTCCA	CCTGCTTCTT	TCTGTGCCCT	TTGGGATTCT	120
GCTTTAGTC	CACCGAAGA	TAACACCTGG	GTGCACTGGA	ACTGTCATGG	GACTATATGC	180
AAAGTGATCT	CGGTGAGCTG	CCTGTGGACG	CAAGATTTCC	TCCTAGAGTG	CCAAAATCTT	240
TTCCATTCAA	CACCTCAGTC	GTGTACAAAA	AGACTCTGTT	TGTAGAATTG	ACGGATCACC	300
TTTTCAACAT	CGCTAACGCC	AGGCCACCC	GGATGGGCTC	GCTAGGTCT	ACCATCCAGG	360
CTGAGGTTTA	TGATACAGTG	GTCATTACAC	TTAAGAACAT	GGCTCCCCAT	CCTGTCAGTC	420
TTCATGCTGT	TGGTGTATCC	TAACGGAAAG	CTTCTGAGGG	AGCTGAATAT	GATGATCAGA	480
CCAGTCAAAG	GGAGAAAGAA	GATGATAAAAG	TCTTCCCTGG	TGGAAGCCAT	ACATATGTCT	540
GGCAGGCTCT	GAAGAGAAAT	GGTCCAAATGG	CCTCTGACCC	ACTGTCCTT	ACCTACTCAT	600
ATCTTCTCA	TGTGGACCTG	GTAAAAGACT	TGAATTCAAGG	CCTCATTGGA	GCCCTACTAG	660
TATGTAGAGA	AGGGAGTCTG	GCCAAAGAAA	AGACACAGAC	CTTGACACAA	TTTATACATAC	720
TTTTGCTGT	ATTGTGATGAA	GGGAAAAGTT	GGCACTCAGA	AACAAAGAAC	TCCTTGATGC	780
AGGATAGGGA	TGCTGCATCT	GCTCGGGCCT	GGCCTAAAAT	GCACACAGTC	AATGGTTATG	840
TAACACAGTC	TCTGCCAGGT	CTGATTGGAT	GCCACAGGAA	ATCAGTCTAT	TGGCATGTGA	900
TTGGAATGGG	CACCACTCCT	GAAGTGCACT	CAATATTCT	CGAAGGTAC	ACATTCTTG	960
TGAGGAACCA	TCGCCAGGCG	TCCTTGGAAA	TCTCGCCAAT	AACTTCTT	ACTGCTCAA	1020
CACTCTTGAT	GGACCTTGGA	CAGTTCTAC	TGTTTTGTCA	TATCTCTTCC	CACCAACATG	1080
ATGGCATGGA	AGCTTATGTC	AAAGTAGACA	GCTGTCCAGA	GGAACCCCAA	CTACGAATGA	1140
AAAATAATGA	AGAACGCGAA	GAATATGATG	ATGATCTTAC	TGATTCTGAA	ATGGATGTGG	1200
TCAGGTTTGA	TGATGACAAC	TCTCCTTCCT	TTATCCTAAAT	TCGCTCAGTT	GCCAAGAAC	1260
ATCCTAAAAC	TTGGGTACAT	TACATTGCTG	CTGAAGAGGA	GGACTGGGAC	TATGCTCCCT	1320
TAGTCCTCGC	CCCCGATGAC	AGAAGTTATA	AAAGTCAATA	TTTGAAACAAT	GGCCCTCAGC	1380
GGATTGGTAG	GAAGTACAAA	AAAGTCCGAT	TTATGGCATA	CACAGATGAA	ACCTTTAAGA	1440
CTCGTGAAGC	TATTTCAGCAT	GAATCAGGAA	TCTTGGGACC	TTTACTTTAT	GGGAAAGTTG	1500
GAGACACACT	GTTGATTATA	TTTAAAGAAC	AAGCAAGCAG	ACCATATAAC	ATCTACCCCTC	1560
ACGGAATCAC	TGATGTCCGT	CCTTTGTATT	CAAGGAGATT	ACCAAAGGT	GTAAAACATT	1620
TGAAGGATTT	TCCAATTCTG	CCAGGAGAAA	TATTCAAATA	TAAATGGACA	GTGACTGTAG	1680
AAGATGGGCC	AACTAAATCA	GATCCTCGGT	GCCTGACCCG	CTATTACTCT	AGTTCTGTTA	1740
ATATGGAGAG	AGATCTAGCT	TCAGGACTCA	TGTTGGCCTCT	CCTCATCTGC	TACAAAGAAC	1800
CTGTAGATCA	AAAGAGGAAAC	CAGATAATGT	CAGACAAGAG	GAATGTCATC	CTGTTTTCTG	1860
TATTTGATGA	GAACCGAAGC	TGGTACCTCA	CAGAGAATAT	ACAACGCTTT	CTCCCCAATC	1920
CAGCTGGAGT	GCAGCTTGAG	GATCCAGAGT	TCCAAGCCTC	CAACATCATG	CACAGCATCA	1980
ATGGCTATGT	TTTGATAGT	TTGCAGTTGT	GAAGTTGT	GCATGAGGTG	GCATACTGGT	2040
ACATTCTAAG	CATTGGGAGCA	CAGACTGACT	TCTCTTCTGT	CTTCTTCTCT	GGATATAACCT	2100
TCAAACACAA	AATGGTCTAT	GAAGACACAC	TCACCCCTATT	CCCATTCTCA	GGAGAAACTG	2160
TCTTCATGTC	GATGGAAAAC	CCAGGTCTAT	GGATTCTGGG	GTGCCACAAC	TCAGACTTTC	2220
GGAACAGAGG	CATGACCGGCC	TTACTGAAGG	TTTCTAGTGTG	TGACAAGAAC	ACTGGTGATT	2280
ATTACGAGGA	CAGTTATGAA	GATATTCAG	CATACTTGCT	GAGTAAAAC	AATGCCATTG	2340
AACCAAGAAG	CTTCTCCCAAG	AACCCACCAG	TCTTGAAACG	CCATCAACGG	GAAATAACTC	2400
GTACTACTCT	TCAGTCAGAT	CAAGAGGAA	TTGACTATGAA	TGATACCATA	TCAGTTGAA	2460
TGAAGAAGGA	AGATTTTGAC	ATTATGATG	AGGATGAAA	TCAGAGCCCC	CGCAGCTTC	2520
AAAAGAAAAC	ACGACACTAT	TTTATTGCTG	CACTGGAGAG	GCTCTGGGAT	TATGGGATGA	2580
GTAGCTCCCC	ACATGTTCTA	AGAAACAGGG	CTCAGAGTGG	CAGTGTCCCT	CAGTTCAAGA	2640
AAGTTGTTTT	CCAGGAATT	ACTGATGGCT	CCTTTACTCA	GCCCTTATAC	CGTGGAGAAC	2700
TAAATGAACA	TTTGGGACTC	CTGGGGCCAT	ATATAAGAGC	AGAAGTTGAA	GATAATATCA	2760
TGGTAACCTT	CAGAAATCAG	GCCTCTCGTC	CCTATTCCCT	CTATTCTAGC	CTTATTTCTT	2820
ATGAGGAAGA	TCAGAGGCAA	GGAGCAGAAC	CTAGAAAAAA	CTTTGTCAAG	CCTAATGAAA	2880
CCAAAACCTA	CTTTTGAA	GTGCAACATC	ATATGGCACC	CACTAAAGAT	GAGTTTGACT	2940
GCAAAGCCTG	GGCTTATTC	TCTGATGTTG	ACCTGGAAA	AGATGTCAC	TCAGGCCCTGA	3000
TTGGACCCCT	TCTGGTCTGC	CACACTAAC	CACTGAACCC	TGCTCATGGG	AGACAAGTGA	3060
CAGTACAGGA	ATTTGCTCTG	TTTTTCACCA	TCTTTGATGA	GACCAAAAGC	TGGTACTTCA	3120
CTGAAAATAT	GGAAAGAAAC	TGCAGGGCTC	CCTGCAATAT	CCAGATGAA	GATCCCACCT	3180
TTAAAGAGAA	TTATCGCTTC	CATGCAATCA	ATGGCTACAT	AATGGATACA	CTACCTGGCT	3240
TAGTAATGGC	TCAGGATCAA	AGGATGCGAT	GGTATCTGCT	CAGCATGGG	AGCAATGAAA	3300
ACATCCATTTC	TATTCATTTC	AGTGGACATG	TGTTCACTGT	ACGAAAAAAA	GAGGAGTATA	3360
AAATGGCACT	GTACAATCTC	TATCCAGGTG	TTTTTGAGAC	AGTGGAAATG	TTACCATCCA	3420
AAGCTGGAAT	TTGGCGGGTG	GAATGCCCTA	TTGGCGAGCA	TCTACATGCT	GGGATGAGCA	3480
CACTTTTCT	GGTGTACAGC	AATAAGTGTG	AGACTCCCC	GGGAATGGCT	TCTGGACACA	3540
TTAGAGATTT	TCAGATTACA	GCTTCAGGAC	AATATGGACA	GTGGGCCCA	AAGCTGGCCA	3600
GACTTCATTA	TTCCGGATCA	ATCAATGCCT	GGAGCACCAA	GGAGCCCTTT	TCTTGGATCA	3660
AGGTGGATCT	GTTGGCACCA	ATGATTATTC	ACGGCATCAA	GACCCAGGGT	GCCCCTCAGA	3720

AGTTCTCCAG	CCTCTACATC	TCTCAGTTA	TCATCATGTA	TAGTCTTGAT	GGGAAGAAGT	3780
GGCAGACTTA	TCGAGGAAT	TCCACTGGAA	CCTTAATGGT	CTTCTTGGC	AATGTGGATT	3840
CATCTGGAT	AAAACACAAT	ATTTTAACC	CTCCAATTAT	TGCTCGATAC	ATCCGTTGC	3900
ACCCAACCTA	TTATAGCATT	CGCAGCACTC	TTCGCATGGA	GTTGATGGC	TGTGATTAA	3960
ATAGTGCAG	CATGCCATTG	GGAATGGAGA	CTAAAGCAAT	ATCAGATGCA	CAGATTACTG	4020
CTTCATCCTA	CTTTACCAAT	ATGTTGCCA	CCTGGTCTCC	TTCAAAAGCT	CGACTTCACC	4080
TCCAAGGGAG	GAGTAATGCC	TGGAGACCTC	AGGTGAATAA	TCCAAAAGAG	TGGCTGCAAG	4140
TGGACTTCCA	GAAGACAATG	AAAGTCACAG	GAGTAACTAC	TCAGGGAGTA	AAATCTCTGC	4200
TTACCAGCAT	GTATGTGAAG	GAGTTCCTCA	TCTCCAGCAG	TCAAGATGGC	CATCAGTGGA	4260
CTCTCTTTT	TCAGAATGGC	AAAGTAAAGG	TTTTTCAGGG	AAATCAAGAC	TCCTTCACAC	4320
CTGTGGTGA	CTCTCTAGAC	CCACCGTTAC	TGACTCGCTA	CCTTCGAATT	CACCCCCAGA	4380
GTTGGGTGCA	CCAGATTGCC	CTGAGGATGG	AGGTTCTGGG	CTGCGAGGCA	CAGGACCTCT	4440
ACTGAGGGTG	CCCAC TGCGCAG	CACCTGCCAC	TGCCGTCA	TCTCCCTCCT	CAGCTCCAGG	4500
GCAGTGTCCC	TCCCTGGCTT	GCCTTCTACC	TTTGTGCTAA	ATCCTAGCAG	ACACTGCCTT	4560
GAAGCCTCCT	GAATTAAC	TCATCAGTCC	TGCATTTCTT	TGGTGGGGGG	CCAGGAGGGT	4620
GCATCCAATT	TAACCTAAC	CTTACCTATT	TTCTGCAGCT	GCTCCCAGAT	TACTCCTTCC	4680
TTCCAATATA	ACTAGGCAA	AAGAAGTGAG	GAGAACCTG	CATGAAAGCA	TTCTCCCTG	4740
AAAAGTTAGG	CCTCTCAGAG	TCACCACTTC	CTCTGTTGTA	GAAAAACTAT	GTGATGAAAC	4800
TTTGAAAAAG	ATATTTATGA	TGTTGCGGCC	GC			4832

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1457 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met	Gln	Ile	Glu	Leu	Ser	Thr	Cys	Phe	Phe	Leu	Cys	Leu	Leu	Arg	Phe
1								5							15

Cys	Phe	Ser	Ala	Thr	Arg	Arg	Tyr	Tyr	Leu	Gly	Ala	Val	Glu	Leu	Ser
								20					25		30

Trp	Asp	Tyr	Met	Gln	Ser	Asp	Leu	Gly	Glu	Leu	Pro	Val	Asp	Ala	Arg
			35				40					45			

Phe	Pro	Pro	Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	Asn	Thr	Ser	Val	Val
				50			55				60				

Tyr	Lys	Lys	Thr	Leu	Phe	Val	Glu	Phe	Thr	Asp	His	Leu	Phe	Asn	Ile
				65			70			75			80		

Ala	Lys	Pro	Arg	Pro	Pro	Trp	Met	Gly	Leu	Leu	Gly	Pro	Thr	Ile	Gln
				85					90				95		

Ala	Glu	Val	Tyr	Asp	Thr	Val	Val	Ile	Thr	Leu	Lys	Asn	Met	Ala	Ser
				100				105				110			

His	Pro	Val	Ser	Leu	His	Ala	Val	Gly	Val	Ser	Tyr	Trp	Lys	Ala	Ser
				115				120			125				

Glu	Gly	Ala	Glu	Tyr	Asp	Asp	Gln	Thr	Ser	Gln	Arg	Glu	Lys	Glu	Asp
				130			135			140					

Asp	Lys	Val	Phe	Pro	Gly	Gly	Ser	His	Thr	Tyr	Val	Trp	Gln	Val	Leu
				145				150			155			160	

Lys	Glu	Asn	Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu	Cys	Leu	Thr	Tyr	Ser
				165					170				175		

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
180 185 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
245 250 255

Val Asn Arg Ser Leu Pro Gly Ile Gly Cys His Arg Lys Ser Val
260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
290 295 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305 310 315 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
325 330 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
340 345 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
370 375 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385 390 395 400

Trp Val His Tyr Ile Ala Ala Glu Glu Asp Trp Asp Tyr Ala Pro
405 410 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
420 425 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
435 440 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
450 455 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465 470 475 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
500 505 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
515 520 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
530 535 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545 550 555 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
565 570 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
580 585 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
595 600 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
610 615 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625 630 635 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
645 650 655

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
660 665 670

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
675 680 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
690 695 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705 710 715 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
725 730 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
740 745 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu
755 760 765

Lys Arg His Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln
770 775 780

Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu
785 790 795 800

Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe
805 810 815

Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp

820

825

830

Asp Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln
835 840 845

Ser Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr
850 855 860

Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His
865 870 875 880

Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile
885 890 895

Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser
900 905 910

Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg
915 920 925

Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val
930 935 940

Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp
945 950 955 960

Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu
965 970 975

Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His
980 985 990

Gly Arg Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe
995 1000 1005

Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys
1010 1015 1020

Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn
1025 1030 1035 1040

Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly
1045 1050 1055

Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met
1060 1065 1070

Gly Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe
1075 1080 1085

Thr Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr
1090 1095 1100

Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile
1105 1110 1115 1120

Trp Arg Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly Met Ser
1125 1130 1135

Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met
1140 1145 1150

Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr
1155 1160 1165

Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile
1170 1175 1180

Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu
1185 1190 1195 1200

Leu Ala Pro Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln
1205 1210 1215

Lys Phe Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu
1220 1225 1230

Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu
1235 1240 1245

Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile
1250 1255 1260

Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His
1265 1270 1275 1280

Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu
1285 1290 1295

Asn Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp
1300 1305 1310

Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp
1315 1320 1325

Ser Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp
1330 1335 1340

Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln
1345 1350 1355 1360

Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu
1365 1370 1375

Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Gln Asp
1380 1385 1390

Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe
1395 1400 1405

Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro
1410 1415 1420

Pro Leu Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His
1425 1430 1435 1440

Gln Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu
1445 1450 1455

Tyr

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr
1 5 10 15

Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu
20 25 30

Ser Lys Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg
35 40 45

His Pro Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Pro Pro Thr Pro
50 55 60

Pro Thr Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg Thr
65 70 75 80

Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser
85 90 95

Val Glu Met Lys
100

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGAGGCATGA	CCGCCTACT	GAAGGTTCT	AGTTGTGACA	AGAACACTGG	TGATTATTAC	60
GAGGACAGTT	ATGAAGATAT	TTCAGCATAC	TTGCTGAGTA	AAAACAATGC	CATTGAACCA	120
AGAAGCTTCT	CCCAGAATTC	TAGACACCCCT	AGCACTAGGC	AAAAGCAATT	TAATGCCACC	180
CCTCCTACAC	CACCAACCCC	ACCAGTACTG	AAACGCCATC	AACGGGAAAT	AACTCGTACT	240
ACTCTTCAGT	CTGATCAAGA	GGAAATTGAC	TATGATGATA	CCATATCAGT	TGAAATGAAG	300

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Ser Arg His Pro Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Pro Pro
1 5 10 15

Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg
20 25

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TCGCGACACC CTAGCACTAG GCAAAAGCAA TTTAATGCCA CCCCCACCAGT CCTGAAACGC
CATCAACGGG AAATAACGCG T

60
81

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACTACTCTTC AATCTGATCA AGAGGAA

27

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CGCGCCGCTC GAGTCTACAA TGGCTTGCC TTTTGCTTTA CTG

43

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCGCCCATCG ATTTATTCTC TCCTCCTTAA CCTTTCTTGC AAG

43

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CGCGCCGCTC GAGCATCCCA ATGGCCCTGT CCTTTCTTT ACTGATGG

48

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CCATCGATTC AATCCTTCCT CCTTAATCTT TTTTGCAAG

39

(2) INFORMATION FOR SEQ ID NO:57:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:
CCGGATCCTC TACAATGGCT TTGCCTTTTG CTTTACTG 38

(2) INFORMATION FOR SEQ ID NO:58:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:
CGCGCCGGCG GCCGCTTATT CCTTCCTCCT TAACCTTTCT TGCAAG 46

(2) INFORMATION FOR SEQ ID NO:59:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:
CCGGATCCCA TCCCAATGGC CCTGTCCCTT TCTTTACTGA TGG 43

(2) INFORMATION FOR SEQ ID NO:60:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
CGCGCCGGCG GCCGCTCAAT CCTTCCTCCT TAATCTTTT TGCAAG 46

(2) INFORMATION FOR SEQ ID NO:61:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:
AGCTTGCTGT TTGTGTGCTG CCTCTGAAGT CCACACTGAA CAAACTTCAG CCTACTCATG 60
TCCCTAAAAT GGGCAACAT TGCAAGCAGC 90

(2) INFORMATION FOR SEQ ID NO:62:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
AACACAGAAA CACACAGCCC TCCCTGCCTG CTGACCTTGG AGCTGGGGCA GAGGTCAGAG 60
ACCTCTCTGA 70

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

AGCTTCAGAG AGGTCTCTGA CCTCTGCCCC AGCTCCAAGG TCAGCAGGCA GGGAGGGCTG 60
TGTGTTTGCT GTTTGCTGCT TG 82

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CAATGTTTGC CCATTTAGG GACATGAGTA GGCTGAAGTT TGTCAGTGT GGACTTCAGA 60
GGCAGCACAC AAACAGCA 78

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

AATTCGCTGT TTGTGTGCTG CCTCTGAAGT CCACACTGAA CAAACTTCAG CCTACTCATG 60
TCCCTAAAT GGGAAACAT TGCAAGCAGC 90

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AAACAGCAAA CACACAGCCC TCCCTGCCTG CTGACCTTGG AGCTGGGGCA GAGGTCAGAG 60
ACCTCTCTGG 70

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

AATTCCAGAG AGGTCTCTGA CCTCTGCCCC AGCTCCAAGG TCAGCAGGCA GGGAGGGCTG 60
TGTGTTTGCT GTTTGCTGCT TG 82

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:
CAATGTTGC CCATTTAGG GACATGAGTA GGCTGAAGTT TGTCAGTGT GGACTTCAGA
GGCAGCACAC AAACAGCG 60
78

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
CGCGCCGCC GGGTAGATC TTGCTACCAAG TGG 33

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:
GCGCCCGCGG CCGCCACTGT CCCAGGTAG TGTTGGTGCC 40

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
CGCGCCGGCG GCCGCTCTAC AATGCCCTTG ACCTTGCTT TACTGG 46

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:
GCGCCCATCG ATTCAATTCT TACTTCTTAA ACTTTCTTGC AAG 43

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:
CGCGCCGGCG GCCGCTCTAC AATGCCCTTG ACCTTGCTT TACTGG 46

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GCGCCCATCG ATTCAATTCT TACTTCTTAA ACTTTCTTGC AAG

43

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Asn Ser Arg His Pro Ser

1 5

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr

1 5 10

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AATTCGCGAC ACCCTAGC

18

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAAAACCCAC CAGTCTTGAAC CGGCCATCAA CGGGAAATAA CG

42

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GCGCTGTGGG ATCGGTTTG GGTGGTCAGA AC

32

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TTTGCAGGTAG TTGCCCTTTA TTGC

24

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Arg Thr Leu Gln Ser Asp

1 5

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CGTACTCTTC AGTCT

15

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GCATGAGAAG TCAGACTAG

19